#9

OIPE

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/805,694B

DATE: 03/18/2002
TIME: 14:50:15

Input Set : A:\REVISED CORRECTED SEQUENCE LISTING BB-1432.txt
Output Set: N:\CRF3\03182002\I805694B.raw

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 3 <110> APPLICANT: Kinney, Anthony
 5 <120> TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
 7 <130> FILE REFERENCE: BB1432 US NA
 9 <140> CURRENT APPLICATION NUMBER: US/09/805,694B
10 <141> CURRENT FILING DATE: 2001-03-14
12 <150> PRIOR APPLICATION NUMBER: 60/189,823
13 <151> PRIOR FILING DATE: 2000-03-16
15 <160> NUMBER OF SEQ ID NOS: 16
17 <170> SOFTWARE: Microsoft Office 97
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1156
21 <212> TYPE: DNA
22 <213> ORGANISM: chimeric construct
24 <400> SEQUENCE: 1
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26 ccagcatatc aactcatcgt tccatattgg accttgacct aaccagtttt accacacaga   120
27 aacaggtgtc ttcactgttc caactatgga agagtgagca tggacgtgtc taccataacc   180
28 acgaagaaga ggcaaagaga cttgagattt tcaagaataa ctcgaactat atcagggaca   240
29 tgaatgcaaa cagaaaatca ccccattctc atcgtttagg attgaacaag tttgctgaca   300
30 tcactcctca agagttcagc aaaaagtact tgcaagctcc caaggatgtg tcgcagcaaa   360
31 tcaaaatggc caacaagaaa atgaagaagg aacaatattc ttgtgaccat ccacctgcat   420
32 catgggattg gaggaaaaaa ggtgtcatca cccaagtaaa gtaccaaggg ggctgtggaa   480
33 ggggttgggc gttttctgcc acgggagcca tagaagcagc acatgcaata gcaacaggag   540
34 accttgttag cctttctgaa caagaactcg tagactgtgt ggaagaaagc gaaggttctt   600
35 acaatggatg gcagtatcaa tcgttcgaat gggtttttaga acatggtggc attgccactg   660
36 atgatgatta tccttacaga gctaaagagg gtagatgcaa agccaataag atacaagaca   720
37 aggttacaat tgacggatat gaaactctaa taatgtcaga tgagagtaca gaatcagaga   780
38 cagagcaagc gttcttaagc gccatccttg agcaaccaat tagtgtctca attgatgcaa   840
39 aagattttca tttatacacc gggggaattt atgatggaga aaactgtaca agtccgtatg   900
40 ggattaatca ctttgtttta cttgtgggtt atggttcagc ggatggtgta gattactgga   960
41 tagcgaaaaa ttcatgggga gaagattggg gagaagatgg ttacatttgg atccaaagaa  1020
42 acacgggtaa tttattagga gtgtgtggga tgaattattt cgcttcatac ccaaccaaag  1080
43 aggaatcaga aacactggtg tctgctcgcg ttaaaggtca tcgaagagtt gatcactctc  1140
44 ctctttgagc ggccgc                                                  1156
46 <210> SEQ ID NO: 2
47 <211> LENGTH: 2970
48 <212> TYPE: DNA
49 <213> ORGANISM: chimeric construct
51 <400> SEQUENCE: 2
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53 taatcagtta cttatccttc ctccatcata attaatcttg gtagtctcga atgccacaac   120
54 actgactagt ctcttggatc ataagaaaaa gccaaggaac aaaagaagac aaaacacaat   180
55 gagagtatcc tttgcatagc aatgtctaag ttcataaaat tcaaacaaaa acgcaatcac   240
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56 acacagtgga catcacttat ccactagctg aatcaggatc gccgcgtcaa gaaaaaaaaa  300
57 ctggacccca aaagccatgc acaacaacac gtactcacaa aggtgtcaat cgagcagccc  360
58 aaaacattca ccaactcaac ccatcatgag ccctcacatt tgttgtttct aacccaacct  420
59 caaactcgta ttctcttccg ccacctcatt tttgtttatt tcaacacccg tcaaactgca  480
60 tgccaccccg tggccaaatg tccatgcatg ttaacaagac ctatgactat aaatatctgc  540
61 aatctcggcc caggttttca tcatcaagaa ccagttcaat atcctagtac accgtattaa  600
62 agaatttaag atatactaac agcggccgca tgggtttcct tgtgttgctt cttttctccc  660
63 tcttaggtct ctcttctagt tccagcatat caactcatcg ttccatattg gaccttgacc  720
64 taaccaagtt taccacacag aaacaggtgt cttcactgtt ccaactatgg aagagtgagc  780
65 atggacgtgt ctaccataac cacgaagaag aggcaaagag acttgagatt ttcaagaata  840
66 actcgaacta tatcagggac atgaatgcaa acagaaaatc accccattct catcgtttag  900
67 gattgaacaa gtttgctgac atcactcctc aagagttcag caaaaagtac ttgcaagctc  960
68 ccaaggatgt gtcgcagcaa atcaaaatgg ccaacaagaa aatgaagaag gaacaatatt 1020
69 cttgtgacca tccacctgca tcatgggatt ggaggaaaaa aggtgtcatc acccaagtaa 1080
70 agtaccaagg gggctgtgga aggggttggg cgttttctgc cacgggagcc atagaagcag 1140
71 cacatgcaat agcaacagga gaccttgtta gcctttctga acaagaactc gtagactgtg 1200
72 tggaagaaag cgaaggttct tacaatggat ggcagtatca atcgttcgaa tgggtttttag 1260
73 aacatggtgg cattgccact gatgatgatt atccttacag agctaaagag ggtagatgca 1320
74 aagccaataa gatacaagac aaggttacaa ttgacggata tgaaactcta ataatgtcag 1380
75 atgagagtac agaatcagag acagagcaag cgttcttaag cgccatcctt gagcaaccaa 1440
76 ttagtgtctc aattgatgca aaagatttttc atttatacac cgggggaatt tatgatggag 1500
77 aaaactgtac aagtccgtat gggattaatc actttgtttt acttgtgggt tatggttcag 1560
78 cggatggtgt agattactgg atagcgaaaa attcatgggg agaagattgg ggagaagatg 1620
79 gttacatttg gatccaaaga aacacgggta atttattagg agtgtgtggg atgaattatt 1680
80 tcgcttcata cccaaccaaa gaggaatcag aaacactggt gtctgctcgc gttaaaggtc 1740
81 atcgaagagt tgatcactct cctctttgag cggccgctac atggccacgt gcatgaagta 1800
82 tgaactaaaa tgcatgtagg tgtaagagct catggagagc atggaatatt gtatccgacc 1860
83 atgtaacagt ataataactg agctccatct cacttcttct atgaataaac aaaggatgtt 1920
84 atgatatatt aacactctat ctatgcacct tattgttcta tgataaattt cctcttatta 1980
85 ttataaatca tctgaatcgt gacggcttat ggaatgcttc aaatagtaca aaaacaaatg 2040
86 tgtactataa gactttctaa acaattctaa ctttagcatt gtgaacgaga cataagtgtt 2100
87 aagaagacat aacaattata atggaagaag tttgtctcca tttatatatt atatattacc 2160
88 cacttatgta ttatattagg atgttaagga gacataacaa ttataaagag agaagtttgt 2220
89 atccatttat atattatata ctacccattt atatattata cttatccact tatttaatgt 2280
90 ctttataagg tttgatccat gatatttcta atattttagt tgatatgtat atgaaagggt 2340
91 actatttgaa ctctcttact ctgtataaag gttggatcat ccttaaagtg ggtctattta 2400
92 attttattgc ttcttacaga taaaaaaaaa attatgagtt ggtttgataa aatattgaag 2460
93 gatttaaaat aataataaat aataaataac atataatata tgtatataaa tttattataa 2520
94 tataacattt atctataaaa aagtaaatat tgtcataaat ctatacaatc gtttagcctt 2580
95 gctggacgac tctcaattat ttaaacgaga gtaaacatat ttgacttttt ggttatttaa 2640
96 caaattatta tttaacacta tatgaaattt ttttttttta tcagcaaaga aataaaatta 2700
97 aattaagaag gacaatggtg tgtcccaatc cttatacaac caacttccac aagaaagtca 2760
98 agtcagagac aacaaaaaaa caagcaaagg aaatttttta atttgagttg tcttgtttgc 2820
99 tgcataattt atgcagtaaa acactacaca taaccctttt agcagtagag caatggttga 2880
100 ccgtgtgctt agcttctttt attttatttt tttatcagca aagaataaat aaaataaaat 2940
101 gagacacttc agggatgttt caacaagctt                                  2970
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 1600
105 <212> TYPE: DNA
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106 <213> ORGANISM: Glycine max
108 <400> SEQUENCE: 3
109 ggggaaacaa aactaccctt ttgcttttgc tctttgttct ttgtcatgga gtggccacaa   60
110 caacaatggc cttccgtgat gatgagggtg gtgataaaaa gtcaccaaaa agtttgtttt  120
111 tgatgagcaa ctccacgagg gttttcaaga ctgatgcagg ggaaatgcgt gtgctgaaaa  180
112 gccatggtgg taggatattt tataggcaca tgcacattgg cttcatctct atggaaccaa  240
113 agtccttgtt tgttcctcag tacctcgact ccaatctcat catattcatc cgtagagggg  300
114 aagcaaagct gggattcata tatgatgatg aactagcgga aaggagattg aagacagggg  360
115 acttgtacat gattccatct ggttcagcat tctatttggt gaacatagga gaaggtcaga  420
116 gacttcacgt tatctgcagc attgacccct ctacaagctt gggattagag accttccagt  480
117 ccttctatat tgggggagga gccaattcgc actcggtgct ttctggattc gaacctgcca  540
118 tccttgaaac tgcatttaat gaatcaagaa cggtggtaga ggaaatcttc tccaaggaac  600
119 tagatgggcc aattatgttc gtggatgatt ctcatgcacc tagcttatgg actaaattcc  660
120 ttcaactgaa gaaggatgac aaagagcaac agctgaagaa aatgatgcaa gaccaagagg  720
121 aggatgagga ggagaagcaa acaagtaggt catggaggaa gctcttggaa accgtatttg  780
122 ggaaggtgaa tgagaagata gagaacaaag acactgctgg ttccccctgcc tcttacaacc  840
123 tctacgatga caaaaaagcc gatttcaaaa acgcttatgg ttggagcaag gcactgcatg  900
124 gaggcgagta tcctccactc agcgaaccgg atattggagt tttacttgtc aaactctcag  960
125 cgggatccat gttggcacct catgtgaatc caatatcaga tgagtatacc atagtgctga 1020
126 gtggttatgg tgaactgcat atagggtatc caaacggaag caaagcaatg aaaactaaaa 1080
127 tcaaacaagg ggacgtgttt gttgtgccaa gatacttccc cttctgtcaa gtagcatcaa 1140
128 gggatggacc cttagagttc tttggcttct ccacttctgc aaggaagaac aagccacagt 1200
129 ttctggctgg tgctgcgtcc cttctaagga ccttgatggg gccggagctt tcggcggcgt 1260
130 tcggagtgag cgaggacacg ttgcggcgcg ctgttgatgc tcagcatgag gctgtgatac 1320
131 tgccatcagc atgggctgca ccaccggaaa atgcagggaa gctgaagatg aagaagagc 1380
132 caaatgctat tagaagcttt gccaatgatg tggttatgga tgttttttaa tttgaacact 1440
133 tgatttggaa tagggggttat ttggtagtgc tagtgcctag tggaattctg tgttgagttt 1500
134 tttgttcttt atatttagtt gagatgtgtg ttgtgttctt gagttgtgaa taaaaatcta 1560
135 ctttctttgt gcarraaaaa aaaaaaaaaa aaaaaaaaaa              1600
137 <210> SEQ ID NO: 4
138 <211> LENGTH: 454
139 <212> TYPE: PRT
140 <213> ORGANISM: Glycine max
142 <400> SEQUENCE: 4
143 Met ala Phe Arg Asp Asp Glu Gly Gly Asp Lys Lys Ser Pro Lys Ser
144  1               5                  10                  15
146 Leu Phe Leu Met Ser Asn Ser Thr Arg Val Phe Lys Thr Asp Ala Gly
147             20                  25                  30
149 Glu Met Arg Val Leu Lys Ser His Gly Gly Arg Ile Phe Tyr Arg His
150         35                  40                  45
152 Met His Ile Gly Phe Ile Ser Met Glu Pro Lys Ser Leu Phe Val Pro
153      50                  55                  60
155 Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe Ile Arg Arg Gly Glu Ala
156  65                  70                  75                  80
158 Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu Ala Glu Arg Arg Leu Lys
159             85                  90                  95
161 Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val
162             100                 105                 110
164 Asn Ile Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro
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165           115               120               125
167 Ser Thr Ser Leu Gly Leu Glu Thr Phe Gln Ser Phe Tyr Ile Gly Gly
168      130               135               140
170 Gly Ala Asn Ser His Ser Val Leu Ser Gly Phe Glu Pro Ala Ile Leu
171 145               150               155               160
173 Glu Thr Ala Phe Asn Glu Ser Arg Thr Val Val Glu Glu Ile Phe Ser
174           165               170               175
176 Lys Glu Leu Asp Gly Pro Ile Met Phe Val Asp Asp Ser His Ala Pro
177           180               185               190
179 Ser Leu Trp Thr Lys Phe Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln
180           195               200               205
182 Gln Leu Lys Lys Met Met Gln Asp Gln Glu Glu Asp Glu Glu Glu Lys
183      210               215               220
185 Gln Thr Ser Arg Ser Trp Arg Lys Leu Leu Glu Thr Val Phe Gly Lys
186 225               230               235               240
188 Val Asn Glu Lys Ile Glu Asn Lys Asp Thr Ala Gly Ser Pro Ala Ser
189           245               250               255
191 Tyr Asn Leu Tyr Asp Asp Lys Lys Ala Asp Phe Lys Asn Ala Tyr Gly
192           260               265               270
194 Trp Ser Lys Ala Leu His Gly Gly Glu Tyr Pro Pro Leu Ser Glu Pro
195           275               280               285
197 Asp Ile Gly Val Leu Leu Val Lys Leu Ser Ala Gly Ser Met Leu Ala
198      290               295               300
200 Pro His Val Asn Pro Ile Ser Asp Glu Tyr Thr Ile Val Leu Ser Gly
201 305               310               315               320
203 Tyr Gly Glu Leu His Ile Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys
204           325               330               335
206 Thr Lys Ile Lys Gln Gly Asp Val Phe Val Val Pro Arg Tyr Phe Pro
207      340               345               350
209 Phe Cys Gln Val Ala Ser Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe
210      355               360               365
212 Ser Thr Ser Ala Arg Lys Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala
213      370               375               380
215 Ser Leu Leu Arg Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly
216 385               390               395               400
218 Val Ser Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Glu Ala
219           405               410               415
221 Val Ile Leu Pro Ser Ala Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys
222      420               425               430
224 Leu Lys Met Glu Glu Glu Pro Asn Ala Ile Arg Ser Phe Ala Asn Asp
225      435               440               445
227 Val Val Met Asp Val Phe
228      450
230 <210> SEQ ID NO: 5
231 <211> LENGTH: 494
232 <212> TYPE: DNA
233 <213> ORGANISM: Glycine max
235 <220> FEATURE:
236 <221> NAME/KEY: unsure
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Output Set: N:\CRF3\03182002\I805694B.raw

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      237 <222> LOCATION: (9)
      238 <223> OTHER INFORMATION: n = A, C, G, or T
      240 <220> FEATURE:
      241 <221> NAME/KEY: unsure
      242 <222> LOCATION: (388)
      243 <223> OTHER INFORMATION: n = A, C, G, or T
      245 <220> FEATURE:
      246 <221> NAME/KEY: unsure
      247 <222> LOCATION: (392)..(393)
      248 <223> OTHER INFORMATION: n = A, C, G, or T
      250 <220> FEATURE:
      251 <221> NAME/KEY: unsure
      252 <222> LOCATION: (460)
      253 <223> OTHER INFORMATION: n = A, C, G, or T
      255 <220> FEATURE:
      256 <221> NAME/KEY: unsure
      257 <222> LOCATION: (463)
      258 <223> OTHER INFORMATION: n = A, C, G, or T
      260 <220> FEATURE:
      261 <221> NAME/KEY: unsure
      262 <222> LOCATION: (468)
      263 <223> OTHER INFORMATION: n = A, C, G, or T
      265 <400> SEQUENCE: 5
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      267 atagctgggt tgtgcttcct cttccttgtt ctctttgttg ctcaagaagt tgtggtgcaa 120
      268 actgaggcaa agacttgcga gaacctggct gatacataca ggggtccatg cttcaccact 180
      269 ggcagctgcg atgatcactg caagaacaaa gagcacttgc tcagaggcag atgcagggac 240
      270 gattttcgct gttggtgcac caaaaactgt taaatggatc cattcactcc aacgtgaaga 300
      271 agatgcatgc agcgctattt tataaaaaat acaactacta tatactatat ataataagac 360
W--> 272 tgggcgctgc atcaatgacc ctatgtanta tnntatatat tattaccgat gtcaagaact 420
W--> 273 atagatgcat gtactgtgca taacggctga gttatgtccn tangttanga ataaaaataa 480
      274 agtgctgttg ttgc                                                   494
      276 <210> SEQ ID NO: 6
      277 <211> LENGTH: 75
      278 <212> TYPE: PRT
      279 <213> ORGANISM: Glycine max
      281 <400> SEQUENCE: 6
      282 Met Glu Lys Lys Ser Ile Ala Gly Leu Cys Phe Leu Phe Leu Val Leu
      283  1               5                  10                  15
      285 Phe Val Ala Gln Glu Val Val Val Gln Thr Glu Ala Lys Thr Cys Glu
      286                 20                  25                  30
      288 Asn Leu Ala Asp Thr Tyr Arg Gly Pro Cys Phe Thr Thr Gly Ser Cys
      289             35                  40                  45
      291 Asp Asp His Cys Lys Asn Lys Glu His Leu Leu Arg Gly Arg Cys Arg
      292         50                  55                  60
      294 Asp Asp Phe Arg Cys Trp Cys Thr Lys Asn Cys
      295 65                  70                  75
      297 <210> SEQ ID NO: 7
      298 <211> LENGTH: 30
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VERIFICATION SUMMARY   DATE: 03/18/2002
PATENT APPLICATION: **US/09/805,694B**   TIME: 14:50:16

Input Set : **A:\REVISED CORRECTED SEQUENCE LISTING BB-1432.txt**
Output Set: **N:\CRF3\03182002\I805694B.raw**

L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5